

OIEP

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/821,255

DATE: 04/17/2001
 TIME: 10:50:51

Input Set : A:\Seqlist.txt
 Output Set: N:\CRF3\04172001\I821255.raw

4 <110> APPLICANT: Michael S.C. Fung
 5 Bill N.C. Sun
 6 Cecily R.Y. Sun
 9 <120> TITLE OF INVENTION: Inhibitors of Complement Activation
 12 <130> FILE REFERENCE: 98-2A
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/821,255
 C--> 14 <141> CURRENT FILING DATE: 2001-03-29
 14 <150> PRIOR APPLICATION NUMBER: 60/075,328
 15 <151> PRIOR FILING DATE: 1998-02-20
 17 <150> PRIOR APPLICATION NUMBER: 09/253,689
 18 <151> PRIOR FILING DATE: 1999-02-20
 20 <160> NUMBER OF SEQ ID NOS: 15
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 699
 26 <212> TYPE: DNA
 27 <213> ORGANISM: human
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (4)...(687)
 33 <400> SEQUENCE: 1
 34 cgg atc ctg ggc ggc aga gag gcc gag gcg cac gcg cgg ccc tac atg 48
 35 Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met
 36 1 5 10 15
 38 gcg tcg gtg cag ctg aac ggc gcg cac ctg tgc ggc ggc gtc ctg gtg 96
 39 Ala Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val
 40 20 25 30
 42 gcg gag cag tgg gtg ctg agc gcg gcg cac tgc ctg gag gac gcg gcc 144
 43 Ala Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala
 44 35 40 45
 46 gac ggg aag gtg cag gtt ctc ctg ggc gcg cac tcc ctg tcg cag ccg 192
 47 Asp Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
 48 50 55 60
 50 gag ccc tcc aag cgc ctg tac gac gtg ctc cgc gca gtg ccc cac ccg 240
 51 Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
 52 65 70 75
 54 gac agc cag ccc gac acc atc gac cac gac ctc ctg ctg cta cag ctg 288
 55 Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Gln Leu
 56 80 85 90 95
 58 tcg gag aag gcc aca ctg ggc cct gct gtg cgc ccc ctg ccc tgg cag 336
 59 Ser Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln
 60 100 105 110
 62 cgc gtg gac cgc gac gtg gca ccg gga act ctc tgc gac gtg gcc ggc 384
 63 Arg Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly
 64 115 120 125
 66 tgg ggc ata gtc aac cac gcg ggc cgc cgc ccg gac agc ctg cag cac 432
 67 Trp Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His

ENTERED

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68      130      135      140
70 gtg ctc ttg cca gtg ctg gac cgc gcc acc tgc aac cgg cgc acg cac      480
71 Val Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His
72      145      150      155
74 cac gac ggc gcc atc acc gag cgc ttg atg tgc gcg gag agc aat cgc      528
75 His Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg
76 160      165      170      175
78 cgg gac agc tgc aag ggt gac tcc ggg ggc ccg ctg gtg tgc ggg ggc      576
79 Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
80      180      185      190
82 gtg ctc gag ggc gtg gtc acc tcg ggc tcg cgc gtt tgc ggc aac cgc      624
83 Val Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
84      195      200      205
86 aag aag ccc ggg atc tac acc cgc gtg gcg agc tat gcg gcc tgg atc      672
87 Lys Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile
88      210      215      220
90 gac agc gtc ctg gcc/tagtaggaat tc      699
91 Asp Ser Val Leu Ala
92      225
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 228
97 <212> TYPE: PRT
98 <213> ORGANISM: human
100 <400> SEQUENCE: 2
101 Ile Leu Gly Gly Arg Glu Ala Glu Ala His Ala Arg Pro Tyr Met Ala
102 1      5      10      15
103 Ser Val Gln Leu Asn Gly Ala His Leu Cys Gly Gly Val Leu Val Ala
104      20      25      30
105 Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Ala Ala Asp
106      35      40      45
107 Gly Lys Val Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
108      50      55      60
109 Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
110 65      70      75      80
111 Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Gln Leu Ser
112      85      90      95
113 Glu Lys Ala Thr Leu Gly Pro Ala Val Arg Pro Leu Pro Trp Gln Arg
114      100      105      110
115 Val Asp Arg Asp Val Ala Pro Gly Thr Leu Cys Asp Val Ala Gly Trp
116      115      120      125
117 Gly Ile Val Asn His Ala Gly Arg Arg Pro Asp Ser Leu Gln His Val
118      130      135      140
119 Leu Leu Pro Val Leu Asp Arg Ala Thr Cys Asn Arg Arg Thr His His
120 145      150      155      160
121 Asp Gly Ala Ile Thr Glu Arg Leu Met Cys Ala Glu Ser Asn Arg Arg
122      165      170      175
123 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
124      180      185      190
125 Leu Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys

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126          195          200          205
127 Lys Pro Gly Ile Tyr Thr Arg Val Ala Ser Tyr Ala Ala Trp Ile Asp
128          210          215          220
129 Ser Val Leu Ala
130 225
132 <210> SEQ ID NO: 3
133 <211> LENGTH: 714
134 <212> TYPE: DNA
135 <213> ORGANISM: pig
137 <220> FEATURE:
138 <221> NAME/KEY: CDS
139 <222> LOCATION: (4)...(702)
141 <400> SEQUENCE: 3
142 cgg\atc ctg ggt ggc cag gag gcc aag tcc cac gag aga ccc tac atg      48
143     Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met
144     1          5          10          15
146 gca tcg gtg cag gtg aac ggc aag cac gtg tgc gga ggc ttc ctg gtg      96
147 Ala Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val
148          20          25          30
150 tct gag cag tgg gtg ctg agt gca gca cac tgc ctg gag gac gtg gcc      144
151 Ser Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala
152          35          40          45
154 gag ggg aag ctg cag gtt ctc ctg ggt gcg cac tcc ctg tca cag ccc      192
155 Glu Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro
156          50          55          60
158 gag ccc tcg aag cgc ctg tac gac gtg ctc cgc gcc gtg ccc cac cca      240
159 Glu Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro
160          65          70          75
162 gac agc cag cct gac acc atc gac cat gat ctc ctc ctg ctg aag ctc      288
163 Asp Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Lys Leu
164 80          85          90          95
166 tcc gag aag gcc gag ctg ggc cct gcc gtg cag ccc ctt gcc tgg caa      336
167 Ser Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln
168          100          105          110
170 cga gag gac cac gag gtt ccg gca ggc acg ctc tgc gac gtg gcc ggc      384
171 Arg Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly
172          115          120          125
174 tgg gga gtg gtc agt cac act ggc cgc cgg ccc gac cgt ctg cag cac      432
175 Trp Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His
176          130          135          140
178 ctg ctc cta ccg gtg ctg gac cgc acc acc tgc aac ctg cgc aca tac      480
179 Leu Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr
180          145          150          155
182 cac gat ggc acc atc acc gag cgc atg atg tgc gcg gag agc aac cgt      528
183 His Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg
184 160          165          170          175
186 cgg gac agc tgc aag ggc gac tcc gga ggc ccg ctg gtg tgc ggg ggt      576
187 Arg Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly
188          180          185          190

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190 gtg gcc gag gga gtg gtt acc tca ggc tcc cga gtc tgc ggc aac cgc      624
191 Val Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg
192                195                200                205
194 aag aaa ccc ggc atc tac acg cgc ttg gcg agc tac gtg gcc tgg atc      672
195 Lys Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile
196                210                215                220
198 gac gga gtg atg gct gac agc gca gcc gcc tagtaggaat tc      714
199 Asp Gly Val Met Ala Asp Ser Ala Ala Ala
200                225                230
203 <210> SEQ ID NO: 4
204 <211> LENGTH: 233
205 <212> TYPE: PRT
206 <213> ORGANISM: pig
208 <400> SEQUENCE: 4
209 Ile Leu Gly Gly Gln Glu Ala Lys Ser His Glu Arg Pro Tyr Met Ala
210 1 5 10 15
211 Ser Val Gln Val Asn Gly Lys His Val Cys Gly Gly Phe Leu Val Ser
212 20 25 30
213 Glu Gln Trp Val Leu Ser Ala Ala His Cys Leu Glu Asp Val Ala Glu
214 35 40 45
215 Gly Lys Leu Gln Val Leu Leu Gly Ala His Ser Leu Ser Gln Pro Glu
216 50 55 60
217 Pro Ser Lys Arg Leu Tyr Asp Val Leu Arg Ala Val Pro His Pro Asp
218 65 70 75 80
219 Ser Gln Pro Asp Thr Ile Asp His Asp Leu Leu Leu Leu Lys Leu Ser
220 85 90 95
221 Glu Lys Ala Glu Leu Gly Pro Ala Val Gln Pro Leu Ala Trp Gln Arg
222 100 105 110
223 Glu Asp His Glu Val Pro Ala Gly Thr Leu Cys Asp Val Ala Gly Trp
224 115 120 125
225 Gly Val Val Ser His Thr Gly Arg Arg Pro Asp Arg Leu Gln His Leu
226 130 135 140
227 Leu Leu Pro Val Leu Asp Arg Thr Thr Cys Asn Leu Arg Thr Tyr His
228 145 150 155 160
229 Asp Gly Thr Ile Thr Glu Arg Met Met Cys Ala Glu Ser Asn Arg Arg
230 165 170 175
231 Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val
232 180 185 190
233 Ala Glu Gly Val Val Thr Ser Gly Ser Arg Val Cys Gly Asn Arg Lys
234 195 200 205
235 Lys Pro Gly Ile Tyr Thr Arg Leu Ala Ser Tyr Val Ala Trp Ile Asp
236 210 215 220
237 Gly Val Met Ala Asp Ser Ala Ala Ala
238 225 230
240 <210> SEQ ID NO: 5
241 <211> LENGTH: 25
242 <212> TYPE: DNA
243 <213> ORGANISM: artificial sequence
245 <220> FEATURE:

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246 <223> OTHER INFORMATION: primer
248 <400> SEQUENCE: 5
249 tgcggccgct gtaggtgctg tcttt                25
251 <210> SEQ ID NO: 6
252 <211> LENGTH: 23
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: primer
259 <400> SEQUENCE: 6
260 ggaattcact cgttattctc gga                23
262 <210> SEQ ID NO: 7
263 <211> LENGTH: 17
264 <212> TYPE: DNA
265 <213> ORGANISM: Artificial Sequence
267 <220> FEATURE:
268 <223> OTHER INFORMATION: primer
270 <400> SEQUENCE: 7
271 tccgagaata acgagtg                17
273 <210> SEQ ID NO: 8
274 <211> LENGTH: 29
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: primer
281 <400> SEQUENCE: 8
282 cattgaaagc ttggggtag aagttgttc        29
284 <210> SEQ ID NO: 9
285 <211> LENGTH: 27
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial Sequence
289 <220> FEATURE:
290 <223> OTHER INFORMATION: primer
292 <400> SEQUENCE: 9
293 cgcgcccgca gctgctcaga gtgtaga        27
295 <210> SEQ ID NO: 10
296 <211> LENGTH: 28
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: primer
303 <400> SEQUENCE: 10
304 cggtaaagctt cactggctca gggaaata        28
306 <210> SEQ ID NO: 11
307 <211> LENGTH: 37
308 <212> TYPE: DNA
309 <213> ORGANISM: Artificial Sequence
311 <220> FEATURE:
312 <223> OTHER INFORMATION: primer

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VERIFICATION SUMMARY

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L:14 M:270 C: Current Application Number differs, Replaced Current Application No

L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date